



## AMENDMENTS

### In the Specification:

Please substitute the following for paragraph 6 beginning on page 5, line 26 and ending on page 6, line 6:

✓ 1 Panel A of Figure 6 depicts the complete DNA sequence and the deduced amino acid sequence (SEQ ID NOS:3-4) of Ag 2160. The nucleotide numbering is shown on the right and amino acid numbering is shown on the left of the sequence. The predicted sequence reveals a possible signal peptide (black overline), 2 potential N-linked glycosylation sites (gray overline), and a single 23-amino acid transmembrane domain (gray frame). Panel B is a Kyte-Doolittle plot of the deduced amino acid sequence. The predicted start and stop codons are also indicated. The putative hydrophobic signal peptide as well as the hydrophobic transmembrane domain are underlined. Panel C is a sequence alignment of Ag 2160 homologues that include mEGP, hEGP-2, hEGP-1 (SEQ ID NOS:5-8). The hydrophobic signal peptide and the hydrophobic transmembrane domain are underlined. The protein sequences are aligned with the type I thyroglobulin sequence repeat (framed). Conserved cysteine residues are in bold type while highly conserved regions are indicated. Panel D is a Northern blot showing the tissue distribution of the Ag 2160 mRNA.

Please substitute the following for paragraph 4 beginning on page 6 line 23 and ending on page 6, line 23:

✓ 2 Figure 10 depicts a partial cDNA clone of Ag 2117 (SEQ ID NOS:1-2) that is recognized by Mab 2117.